NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length or a pair of primers selected from the group consisting of
VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63);
VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and
VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

74. A method for determining the presence of a nucleic acid according claim 60 within the genetic make-up of a plant, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length, or a pair of primers selected from the group consisting of
VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63);
VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and
VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

75. A method according to claim 73, which comprises the steps of:

(a) providing a preparation of nucleic acid from a plant cell;

(b) providing a nucleic acid molecule which is a probe, said probe comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and

at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said probe is 15 to 40 nucleotides in length;

(c) contacting nucleic acid in said preparation with said probe under conditions for hybridisation; and

(d) identifying a nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7, if present by its hybridisation with said nucleic acid probe.

76. A method according to claim 73, which method comprises the steps of:

(a) providing a preparation of nucleic acid from a plant cell;

(b) providing a pair of nucleic acid molecule primers suitable for PCR, at least one of said primers being a primer which comprises a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length;

(c) contacting nucleic acid in said preparation with said primers under conditions for performance of PCR;

(d) performing PCR and determining the presence or absence of an amplified PCR product.

77. A method according to claim 76 wherein the pair of nucleic acid molecule primers are
VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63);
VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and
VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

78. A method of selecting a plant having a desired allele of the VRN2 gene, which method employs a probe or primer, said

probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length, or a pair of primers selected from the group consisting of
VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63);
VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and
VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

B3 Cancel

Response to Claim Objections

At the outset, the Examiner has objected to the claims for not incorporating SEQ ID NO's. In response, the claims have been amended to include sequence identifiers as required. Accordingly, this objection is believed overcome.

Next, the Examiner has requested that pages 6, 8, and 10 of the preliminary amendment filed November 21, 2001 be resubmitted. In response to this requirement, these pages are attached herewith as Appendix C.

Traversal of Restriction Requirement

In the Requirement for Restriction under 35 U.S.C. §121 and §372 set forth in the Official Action dated March 21, 2003, in the above-identified application it is the Examiner's position that the inventions are not so linked as to form a single general inventive concept under PCT Rule 13.1, and that the inventions must be restricted to the following Groups:

It is the Examiner's position that the application describes fourteen (14) distinct inventions. These are as follows:

Group I, claims 1-4, 60-65, 72-75, and 78 drawn to an isolated nucleic acid of SEQ ID NO: 1 from the VRN2 locus of a

plant encoding SEQ ID NO: 2 and to a method of identifying or cloning a nucleic acid comprising hybridizing a probe to the nucleic acid molecule;

Group II, claims 1, 2, 5, 6, 60-65, 72-75, and 78 drawn to an isolated nucleic acid sequence of SEQ ID NO: 4 from the VRN2 locus of a plant encoding SEQ ID NO: 5 and to a method of identifying or cloning a nucleic acid comprising hybridizing a probe to the nucleic acid molecule;

Herein, the Examiner notes that claims 1 and 2 link inventions I and II. The Examiner adds that the restriction requirement between Groups I and II will be withdrawn upon the allowance of linking claims 1 and 2.

Group III, claims 7, 8, 60-65, 72-75, and 78 drawn to an isolated nucleic acid of SEQ ID NO: 7 from the VRN2 locus of a plant encoding SEQ ID NO: 8 and to a method of identifying or cloning a nucleic acid comprising hybridizing a probe to the nucleic acid molecule;

Group IV, claims 9-10, 60-65, 72-75, and 78 drawn to an isolated nucleic acid obtainable from the VRN2 locus of a plant and to a method of identifying or cloning a nucleic acid comprising hybridizing a probe to a nucleic acid molecule;

Group V, claims 66-70 drawn to an isolated nucleic acid for use as a probe or primer;

Group VI, claim 71 drawn to a process for producing a nucleic acid;

Group VII, claims 72-74 and 76-78 drawn to a method of identifying or cloning a nucleic acid comprising PCR;

Group VIII, claims 79-92 drawn to a recombinant vector comprising a nucleotide sequence and promoter, transformed host cell, and transgenic plant;

Group IX, claims 93-99 and 104, drawn to an isolated polypeptide;

Group X, claims 100-101 drawn to an isolated nucleic acid encoding a fragment of SEQ ID NO: 2, 5, or 8;

Group XI, claim 102 drawn to a method of making the polypeptide of SEQ ID NO: 2, 5, or 8;

Group XII, claim 103 drawn to an antibody;

Group XIII, claim 105 drawn to a method for affecting a physical characteristic of a plant comprising allowing transcription from a nucleic acid; and

Group XIV, claim 106 drawn to a method of reducing VRN2 expression by co-suppression.

Additionally, the Examiner requires the election of specific SEQ ID NOs with the election of Group IV, V, VI, VII, VIII, IX, X, or XIV.

The Examiner also asserts that the claims are not linked by a single special technical feature because Group XIII is allegedly taught by Chandler et al. (The Plant Journal, 1996, 10(4):637-644). Specifically, the Examiner alleges that Chandler et al. provide endogenous mutant *vrn* genes which would comprise a nucleic acid sequence that is a fragment of any of the sequences listed in claim 105.

Election with Traverse

In order to be fully responsive to the above-mentioned requirement, Applicant hereby elects, with traverse, Group I, Claims 1-4, 60-65, 72-75, and 78, drawn to an isolated nucleic acid of SEQ ID NO:1 from the VRN2 locus of a plant encoding SEQ ID NO:2, and to a method of identifying or cloning a nucleic acid comprising hybridizing a probe to a nucleic acid molecule.

Traversal

Applicants respectfully traverse this restriction requirement for the following reasons. First, it is improper to make a lack of unity holding in a §371 application, when the international application was found to have unity. Second, the rules for unity of invention have been improperly applied by the US Examiner. Finally, the restriction requirement is contrary to standard US practice.

First, applicants respectfully submit that the restriction requirement set forth above is improper for failure to comply with the relevant provisions of the Manual of Patent Examining Procedure (M.P.E.P.) pertaining to unity of invention determinations. The present application was filed under 35 U.S.C. §371 as a U.S. national stage application under the Patent Cooperation Treaty.

As stated in § 1893.03(d) of the M.P.E.P.:

> Examiners are reminded that unity of invention (not restriction) practice is applicable in international applications (both Chapter I and II) and in national stage applications submitted under 35 U.S.C. § 371...
>
> The principles of unity of invention are used to determine the types of claimed subject matter and the combinations of claims to different categories of invention that are permitted to be included in a single international or national stage patent application. The basic principle is that an application should relate to only one invention or, if there is more than one invention, that applicant would have a right to include in a single application only those inventions which are so

> linked as to form a single general inventive concept.
>
> A group of inventions is considered linked to form a single general inventive concept where there is a technical relationship among the inventions that involves at least one common or corresponding special technical feature. The expression special technical features is defined as meaning those technical features that define the contribution which each claimed invention, considered as a whole, makes over the prior art.... Note also examples 1-17 of Annex B Part 2 of the PCT Administrative Instructions as amended 01 July 1992 contained in Appendix AI of the M.P.E.P.

In particular, note Example 17 of the Annex, which is highly relevant to biotechnology applications:

> ***Example 17***
> Claim 1: Protein X.
> Claim 2: DNA sequence encoding protein X.
> Expression of the DNA sequence in a host results in the production of a protein which is determined by the DNA sequence. The protein and the DNA sequence exhibit corresponding special technical features. Unity between claims 1 and 2 is accepted.

In view of these rules, it is noteworthy that during the international stage of this application, in the International Search Report issued June 20, 2000, the Examiner did not make a lack of unity finding, and considered all of the claims to be directed to a single invention. This is particularly relevant, since the Chandler (1996) reference was before the Examiner at the time.

Plainly, the restriction requirement of March 21, 2003 fails to comply with the established United States Patent and Trademark Office practice of following the international rules regarding unity of invention in the prosecution of applications filed under § 371.

It is therefore unclear how the Examiner could conclude that instant application has fourteen Groups of inventions, when the international application from which it originates has unity of invention.

Second, even if it was proper to make a lack of unity

holding in the face of unity in the international application, the Examiner has improperly applied the rules for unity of invention. These reasons are set forth point by point below.

1. Chandler, cited by the Examiner as evidence of lack of a unifying concept, has been improperly cited. The reasons that the instant claims are novel and inventive over Chandler (1996) are twofold.

The Examiner's Groups I and II relate to VRN2 cDNA and amino acid sequences SEQ IDs 1-2 (*Arabidopsis thaliana* Landsberg erecta) and SEQ IDs 4-5 (*Arabidopsis thaliana* Columbia).

These are unified by a common inventive concept (actually recited in claims 1 and 2) namely isolated VRN2 nucleic acid, which the present invention provides for the first time.

The alleged rationale for the lack of unity appears to be set out in the action page 6, section 4 - namely that Chandler (1996) discloses a fragment of a sequence recited in claim 105. However this argument is unfounded for two reasons:

First, Chandler (1996) (which is the earlier work of one of the present inventors) **does not** relate to the actual cloning and transcription of VRN2 or even a fragment thereof, as the Examiner seems to imply. It does disclose mutagenesis, mapping, and RNA analysis, but none of these things falls within the scope of claim 105 as worded. Therefore applicants submit that Chandler (1996) does not affect the novelty of this claim, a position which is consistent with that taken by the Examiner during IPE, in which all claims were accepted as novel, including with respect to Chandler (1996).

Second, even if Chandler (1996) did affect claim 105 (which it absolutely does not), this is irrelevant to claims 1 and 2, and the inventive concept which unifies the various groups defined by the Examiner - the provision of isolated VRN2 nucleic acid, and corresponding uses and materials based on the same.

Thus it is clear that the special technical feature which

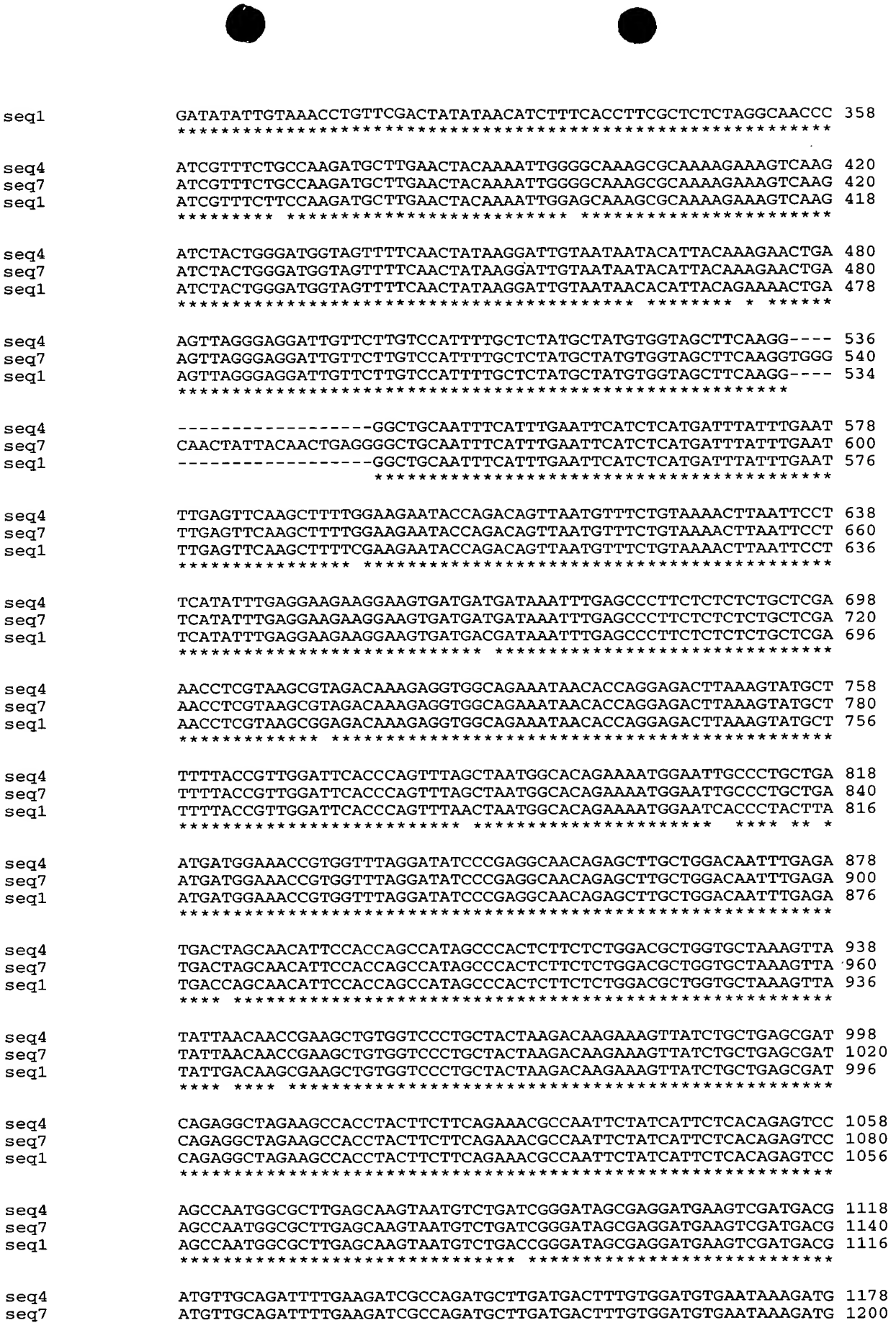
links these claims (an isolated VRN2 nucleic acid) defines a contribution over the prior art, and this feature is embodied as an essential feature of all Groups defined by the Examiner. The restriction requirement is therefore improper under R 13.1 and R13.2 PCT, which again is consistent with the position taken by ISR, who were applying the same criteria, and who were also aware of Chandler (1996).

2. Comments made at section 5. of the examiner's action are entirely irrelevant to the unity of invention test of R13.1 and R13.2 PCT. Of course all different nucleic acids are (by definition) structurally distinct. However the claimed VRN2 sequences are not "unrelated to each" - rather they are all closely related in terms of both structure and function (in terms of the function of the VRN2 polypeptide).

Indeed, the VRN2 cDNA sequences from *Arabidopsis thaliana* Landsberg erecta and *Arabidopsis thaliana* Columbia (SEQ ID NOS. 1 and 4, respectively) show 96% identity as determined by BLASTN. Further, an alignment of the VRN2 sequences of SEQ ID NOs. 1, 4, and 7 clearly demonstrates the structural similarity of the sequences:

Alignment of SEQ ID Nos. 1, 4, and 7

```
seq4        CAAGCTTCTTCAATTTTGCTTGCTCTCTCTCTTACACGGCCAATCGGTGTTTTCGCAGCT 60
seq7        CAAGCTTCTTCAATTTTGCTTGCTCTCTCTCTTACACGGCCAATCGGTGTTTTCGCAGCT 60
seq1        CAAGCTTCTTCAATTTTGCTTGCTCTCTCT--TACACAGCCAATCGGTGTTTTCGCAGCT 58
            ******************************  ***** ********************** 

seq4        TTCAGGCCTCAATACAAGACATTCTATATAAGCATATTGCAGAAGAGGCGGTTCTAATTG 120
seq7        TTCAGGCCTCAATACAAGACATTCTATATAAGCATATTGCAGAAGAGGCGGTTCTAATTG 120
seq1        TTCAGGCCTCAATCCAAGACATTCTATATAAGCATATTGCAGAAGAGGCGGTTCTAATTG 118
            ************ ************************************************ 

seq4        TTGCATGGAGTTGAACAATATGACGTAGGGAAATTCTAATTTAGGGGAGGCCTCAGAGTT 180
seq7        TTGCATGGAGTTGAACAATATGACGTAGGGAAATTCTAATTTAGGGGAGGCCTCAGAGTT 180
seq1        TTGCATTGAGTTTATCGCTATGACGTAGGGAAATTCTAATTTAGGGGAGGCCTCAGAGTT 178
            ****** ***** * *  ****************************************** 

seq4        TGCACTAACTTCATAATCAGCTCTGGACGTTGTTGATTGTATTTGAACAAGAATGTGTAG 240
seq7        TGCACTAACTTCATAATCAGCTCTGGACGTTGTTGATTGTATTTGAACAAGAATGTGTAG 240
seq1        TGCACTAACTTCATAATCGGCTCTTGACGTTGTTGAGTGTAATTGAACAAGAATGTGTAG 238
            ****************** ***** ************ **** ****************** 

seq4        GCAGAATTGTCGCGCGAAATCCTCACCGGAGGAAGTGATTTCAACTGATGAGAATCTCTT 300
seq7        GCAGAATTGTCGCGCGAAATCCTCACCGGAGGAAGTGATTTCAACTGATGAGAATCTCTT 300
seq1        GCAGAATTGTCGCGCGAAATCCTCACCGGAGGAAGTGATTTCAACTGATGAGAATCTCTT 298
            ************************************************************ 

seq4        GATATATTGTAAACCTGTTCGACTATATAACATCTTTCACCTTCGCTCTCTAGGCAACCC 360
seq7        GATATATTGTAAACCTGTTCGACTATATAACATCTTTCACCTTCGCTCTCTAGGCAACCC 360
```


seq1 GATATATTGTAAACCTGTTCGACTATATAACATCTTTCACCTTCGCTCTCTAGGCAACCC 358
seq4 ATCGTTTCTGCCAAGATGCTTGAACTACAAAATTGGGGCAAAGCGCAAAAGAAAGTCAAG 420
seq7 ATCGTTTCTGCCAAGATGCTTGAACTACAAAATTGGGGCAAAGCGCAAAAGAAAGTCAAG 420
seq1 ATCGTTTCTTCCAAGATGCTTGAACTACAAAATTGGAGCAAAGCGCAAAAGAAAGTCAAG 418
seq4 ATCTACTGGGATGGTAGTTTTCAACTATAAGGATTGTAATAATACATTACAAAGAACTGA 480
seq7 ATCTACTGGGATGGTAGTTTTCAACTATAAGGATTGTAATAATACATTACAAAGAACTGA 480
seq1 ATCTACTGGGATGGTAGTTTTCAACTATAAGGATTGTAATAACACATTACAGAAAACTGA 478
seq4 AGTTAGGGAGGATTGTTCTTGTCCATTTTGCTCTATGCTATGTGGTAGCTTCAAGG---- 536
seq7 AGTTAGGGAGGATTGTTCTTGTCCATTTTGCTCTATGCTATGTGGTAGCTTCAAGGTGGG 540
seq1 AGTTAGGGAGGATTGTTCTTGTCCATTTTGCTCTATGCTATGTGGTAGCTTCAAGG---- 534
seq4 ------------------GGCTGCAATTTCATTTGAATTCATCTCATGATTTATTTGAAT 578
seq7 CAACTATTACAACTGAGGGGCTGCAATTTCATTTGAATTCATCTCATGATTTATTTGAAT 600
seq1 ------------------GGCTGCAATTTCATTTGAATTCATCTCATGATTTATTTGAAT 576
seq4 TTGAGTTCAAGCTTTTGGAAGAATACCAGACAGTTAATGTTTCTGTAAAACTTAATTCCT 638
seq7 TTGAGTTCAAGCTTTTGGAAGAATACCAGACAGTTAATGTTTCTGTAAAACTTAATTCCT 660
seq1 TTGAGTTCAAGCTTTTCGAAGAATACCAGACAGTTAATGTTTCTGTAAAACTTAATTCCT 636
seq4 TCATATTTGAGGAAGAAGGAAGTGATGATGATAAATTTGAGCCCTTCTCTCTCTGCTCGA 698
seq7 TCATATTTGAGGAAGAAGGAAGTGATGATGATAAATTTGAGCCCTTCTCTCTCTGCTCGA 720
seq1 TCATATTTGAGGAAGAAGGAAGTGATGACGATAAATTTGAGCCCTTCTCTCTCTGCTCGA 696
seq4 AACCTCGTAAGCGTAGACAAAGAGGTGGCAGAAATAACACCAGGAGACTTAAAGTATGCT 758
seq7 AACCTCGTAAGCGTAGACAAAGAGGTGGCAGAAATAACACCAGGAGACTTAAAGTATGCT 780
seq1 AACCTCGTAAGCGGAGACAAAGAGGTGGCAGAAATAACACCAGGAGACTTAAAGTATGCT 756
seq4 TTTTACCGTTGGATTCACCCAGTTTAGCTAATGGCACAGAAAATGGAATTGCCCTGCTGA 818
seq7 TTTTACCGTTGGATTCACCCAGTTTAGCTAATGGCACAGAAAATGGAATTGCCCTGCTGA 840
seq1 TTTTACCGTTGGATTCACCCAGTTTAACTAATGGCACAGAAAATGGAATCACCCTACTTA 816
seq4 ATGATGGAAACCGTGGTTTAGGATATCCCGAGGCAACAGAGCTTGCTGGACAATTTGAGA 878
seq7 ATGATGGAAACCGTGGTTTAGGATATCCCGAGGCAACAGAGCTTGCTGGACAATTTGAGA 900
seq1 ATGATGGAAACCGTGGTTTAGGATATCCCGAGGCAACAGAGCTTGCTGGACAATTTGAGA 876
seq4 TGACTAGCAACATTCCACCAGCCATAGCCCACTCTTCTCTGGACGCTGGTGCTAAAGTTA 938
seq7 TGACTAGCAACATTCCACCAGCCATAGCCCACTCTTCTCTGGACGCTGGTGCTAAAGTTA 960
seq1 TGACCAGCAACATTCCACCAGCCATAGCCCACTCTTCTCTGGACGCTGGTGCTAAAGTTA 936
seq4 TATTAACAACCGAAGCTGTGGTCCCTGCTACTAAGACAAGAAAGTTATCTGCTGAGCGAT 998
seq7 TATTAACAACCGAAGCTGTGGTCCCTGCTACTAAGACAAGAAAGTTATCTGCTGAGCGAT 1020
seq1 TATTGACAAGCGAAGCTGTGGTCCCTGCTACTAAGACAAGAAAGTTATCTGCTGAGCGAT 996
seq4 CAGAGGCTAGAAGCCACCTACTTCTTCAGAAACGCCAATTCTATCATTCTCACAGAGTCC 1058
seq7 CAGAGGCTAGAAGCCACCTACTTCTTCAGAAACGCCAATTCTATCATTCTCACAGAGTCC 1080
seq1 CAGAGGCTAGAAGCCACCTACTTCTTCAGAAACGCCAATTCTATCATTCTCACAGAGTCC 1056
seq4 AGCCAATGGCGCTTGAGCAAGTAATGTCTGATCGGGATAGCGAGGATGAAGTCGATGACG 1118
seq7 AGCCAATGGCGCTTGAGCAAGTAATGTCTGATCGGGATAGCGAGGATGAAGTCGATGACG 1140
seq1 AGCCAATGGCGCTTGAGCAAGTAATGTCTGACCGGGATAGCGAGGATGAAGTCGATGACG 1116
seq4 ATGTTGCAGATTTTGAAGATCGCCAGATGCTTGATGACTTTGTGGATGTGAATAAAGATG 1178
seq7 ATGTTGCAGATTTTGAAGATCGCCAGATGCTTGATGACTTTGTGGATGTGAATAAAGATG 1200

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seq1        ATGTTGCAGATTTTGAAGATCGCCAGATGCTTGATGACTTTGTGGATGTGAATAAAGATG 1176
            ************************************************************

seq4        AAAAGCAATTCATGCATCTTTGGAACTCGTTTGTAAGAAAACAAAGGGTTATAGCAGATG 1238
seq7        AAAAGCAATTCATGCATCTTTGGAACTCGTTTGTAAGAAAACAAAGGGTTATAGCAGATG 1260
seq1        AAAAGCAATTCATGCATCTTTGGAACTCGTTTGTAAGAAAACAAAGGGTTATAGCAGATG 1236
            ************************************************************

seq4        GTCATATCTCTTGGGCATGTGAAGTATTTTCAAGATTTTACGAGAAAGAGTTGCACTGTT 1298
seq7        GTCATATCTCTTGGGCATGTGAAGTATTTTCAAGATTTTACGAGAAAGAGTTGCACTGTT 1320
seq1        GTCATATCTCTTGGGCATGTGAAGCATTTTCAAGATTTTACGAGAAAGAGTTGCACCGTT 1296
            ************************ ********************************** ***

seq4        ACTCATCACTCTTCTGGTGTTGGAGATTGTTTTTGATTAAACTATGGAACCATGGACTTG 1358
seq7        ACTCATCACTCTTCTGGTGTTGGAGATTGTTTTTGATTAAACTATGGAACCATGGACTTG 1380
seq1        ACTCATCACTCTTCTGGTGTTGGAGATTGTTTTTGATTAAACTATGGAACCATGGACTTG 1356
            ************************************************************

seq4        TCGACTCAGCCACCATCAACAACTGCAATACCATCCTCGAGAATTGCCGTAATACCTCAG 1418
seq7        TCGACTCAGCCACCATCAACAACTGCAATACCATCCTCGAGAATTGCCGTAATACCTCAG 1440
seq1        TCGACTCAGCCACCATCAACAACTGCAATACCATCCTCGAGAATTGCCGTAATAGCTCAG 1416
            ********************************************************* *****

seq4        ------TCACTAACAACAACAACAACAGTGTGGATCATCCCAGTGACTCAAACACCAACA 1472
seq7        ------TCACTAACAACAACAACAACAGTGTGGATCATCCCAGTGACTCAAACACCAACA 1494
seq1        ACACCACCACCACCAACAACAACAACAGTGTGGATCGTCCCAGTGACTCAAACACCAACA 1476
                  *** * ************************ ************************

seq4        ACAATAACATTGTGGATCATCCGAATGACATAAAAAACAAGAACAATGTTGACAACAAGG 1532
seq7        ACAATAACATTGTGGATCATCCGAATGACATAAAAAACAAGAACAATGTTGACAACAAGG 1554
seq1        ACAATAACATTGTGGATCATCCCAATGACATAAACAACAAGAACAATGTTGACAACAAGG 1536
            ********************** *********** *************************

seq4        ACAATAACAGCAGAGACAA-GTAATTAAATAGGAAACACTCCGGTTTAGATGATACCGAT 1591
seq7        ACAATAACAGCAGAGACAA-GTAATTAAATAGGAAACACTCCGGTTTAGATGATACCGAT 1613
seq1        ACAATAACAGCAGAGACAAAGTAATTAAATAGGAAAATCTCCGGCTTTTATGATACCGAT 1596
            ******************* ***************  ****** **  ***********

seq4        CTATCGGATTGTAACTTATTCTTCTTTCTTAAAAAAATTGTTTAGGAGCAAACAAAGATT 1651
seq7        CTATCGGATTGTAACTTATTCTTCTTTCTTAAAAAAATTGTTTAGGAGCAAACAAAGATT 1673
seq1        TTATCGGATTGTAACTTATTCTTCTTTCTTAAAAAA-TTGTTTAGGAGCAAACAAATTTT 1655
             ********************************** ******************  **

seq4        TTATTTGTTAGTGTATTCAACTGATTACATTTTTAGTTAAAAAAA----TGGATTCTCCT 1707
seq7        TTATTTGTTAGTGTATTCAACTGATTACATTTTTAGTTAAAAAAA----TGGATTCTCCT 1729
seq1        TTATATGTTAGTGTATTCAACTGATTACATTTTTAGTTAAAAAAAAAAATGGATTCTGCT 1715
            **** ****************************************    ******** **

seq4        TAATAACT 1715
seq7        TAATAACT 1737
seq1        TA-TAACT 1722
            ** *****
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Further, SEQ ID NOs 3 and 6 are genomic sequences of the cDNA's of SEQ ID NO:1 and 4 (see pages 45-46 of the published application.) Thus these sequences also contain large regions of homology. Therefor applicants submit that these sequences are so similar that they should be examined together.

3. The MPEP sets out specific rules for examination of nucleotide sequences for international and 371 applications. See MPEP 1850:

> UNITY OF INVENTION - NUCLEOTIDE SEQUENCES
> Under 37 CFR 1.475 and 1.499 et seq., when claims do not comply with the requirement of unity of invention, i.e., when the claimed subject matter does not involve "one or more of the same or corresponding special technical features," 37 CFR 1.475(a), an additional fee is required to maintain the claims in the same application. 37 CFR 1.476 (b).
>
> The Commissioner has decided sua sponte to partially waive 37 CFR 1.475 and 1.499 et seq. to permit applicants to claim up to ten (10) nucleotide sequences that do not have the same or corresponding special technical feature without the payment of an additional fee. The PCT permits inventions that lack unity of invention to be maintained in the same international application for payment of additional fees. Thus, in international applications, for each group for which applicant has paid additional international search and/or preliminary examination fees, the USPTO has determined that up to four (4) such additional sequences per group is a reasonable number for examination. Further, claims directed to the selected sequences will be examined with claims drawn to any sequence combinations which have a common technical feature with the selected sequences. Nucleotide sequences encoding the same protein are considered to satisfy the unity of invention standard and will continue to be examined together.

Applicants again submit that there was unity of invention in the international stage of the instant application, and further, that all of the sequences in question share a common, novel special technical feature. Further, as indicated above, multiple, related nucleotide sequences should be examined together. Therefor, all of the nucleotides in the instant application should be considered.

4. The question of whether sequences (or other aspects of the invention) which appear in dependent claims may be patentably distinct is also expressly irrelevant to the criterion of unity under R13.1 and 13.2 PCT (see R13.4PCT).

Thus all claims dependent on claim 1 or 2 should be rejoined (see Annex B in the PCT administrative instructions, attached hereto as Appendix B).

In particular:

Group III

Group III concerns VRN2 cDNA and amino acid sequences SEQ IDs 7-8 (*Arabidopsis thaliana* Columbia splice variant) - see page 45 of the published application - this shares the same inventive concept discussed above as inter alia SEQ ID NO:1-2. It should also be rejoined with Group I.

Group IV

Group IV concerns isolated VRN2 gDNA SEQ IDs 3 (*Arabidopsis thaliana* Landsberg erecta) and 6 (*Arabidopsis thaliana* Columbia) - see page 45 of the published application. These share the same inventive concept as inter alia SEQ ID NO:1, and should also be rejoined with Group I.

Groups V and X

These Groups (probes and primers, other related nucleic acids, including complement nucleic acid) are also concerned with the special technical feature which links these claims - isolated VRN2 nucleic acid, which feature is an essential feature of the claims. They should also be rejoined with Group I.

Groups VI and VII

It is set out in the PCT applicant's guide (also Annex B in the PCT administrative instructions (Appendix B), or in MPEP 1850) that processes for manufacture of a product are construed as sharing the inventive concept with that product. Hence these groups should also be rejoined with the products defined in Group I (and other Groups discussed above). In any case these groups also recite the special technical features which link the claims i.e. are based on isolated VR2 nucleic acid.

Group VIII

This group (vectors, cells, etc.) is also concerned explicitly with the special technical feature which links these claims - isolated VRN2 nucleic acid, which feature is an essential feature of the claims. It should be rejoined with Group I.

Group IX

The nucleic acid claims (Group I) and polypeptide claims (Group IX) have unity of invention because they share a "special technical relationship". In particular the special technical feature which they share is the sequence of amino acids in the peptides which is an essential structural element of the peptides which is encoded by an exactly corresponding sequence of codons.

Group XI and XIII and IV

It is set out in the PCT applicant's guide (also Annex B in the PCT administrative instructions (Appendix B) or in MPEP 1850) that uses of a product are construed as sharing the inventive concept with that product. Hence these groups should also be rejoined with the products defined in Group I (and other Groups discussed above). In any case these groups also recite the special technical features which link the claims (i.e. are based on isolated VRN2 nucleic acid).

5. Further, it is noted that linking claim practice applied by the Examiner to Groups I and II is only pertinent to cases filed under §111, and should not properly be included in the instant case, which was filed under §371.

Therefore, for all of the reasons set forth above, it is clear that the Examiner has not properly applied the rules of unity of invention.

Finally, it is respectfully submitted that even if the current claims did lack a special technical feature (which they certainly don't), all of the claims of Groups I-V,

VIII, X, and XI should be grouped together. The reasoning for this is that in the United States, one criteria for restriction, regardless of whether the application is filed under §111 or §371 is that the claims which are divided must be patentably distinct, and must not raise double patenting issues over each other. See MPEP 804.01:

> 35 U.S.C. 121 authorizes the Commissioner to restrict the claims in a patent application to a single invention when independent and distinct inventions are presented for examination. **The third sentence of 35 U.S.C. 121 prohibits the use of a patent issuing on an application with respect to which a requirement for restriction has been made, or on an application filed as a result of such a requirement, as a reference against any divisional application, if the divisional application is filed before the issuance of the patent.** *Emphasis added*

It is applicant's understanding that this is the reason that in all US cases, regardless of the statute they were filed under, it is customary to include the polynucleotide, vector, host cell, and method of making a protein using the same in one group. In light of these points Applicants submit that at minimum, Groups I-V, VIII, X, and XI should be rejoined, as these are all drawn to polynucleotides, vectors and host cells which comprise the polynucleotides, and methods of making a polypeptide by expressing the same.

Applicants hereby reserve the right to file one or more continuing applications, as provided in 35 U.S.C. §120, on the subject matter of any claims finally held withdrawn from consideration in this application.

Early and favorable action on the merits of this application is respectfully solicited.

Respectfully submitted,
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Enclosures: Appendix A, B, and C